

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Carter, Kenneth C.
He, Wei-Wu
- (ii) TITLE OF INVENTION: Human NK-3 Related Prostate Specific
Gene-1
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVE., NW, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/105,470
 - (B) FILING DATE: 26-JUN-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/051,080
 - (B) FILING DATE: 27-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0790001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 301-309-8504
 - (B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCTCAGGG TTCCGGAGCC GCGGCCCGGG GAGGCGAAAG CGGAGGGGGC CGCGCCGCCG

ACCCCGTCCA AGCCGCTCAC GTCCTTCCTC ATCCAGGACA TCCTGCGGGA CGGCGCGCAG 120
 CGGCAAGGCG GCCGCACGAG CAGCCAGAGA CAGCGCGACC CGGAGCCGGA GCCAGAGCCA 180
 GAGCCAGAGG GAGGACGCAG CCGCGCCGGG GCGCAGAACG ACCAGCTGAG CACCGGGCCC 240
 CGCGCCGCGC CGGAGGAGGC CGAGACGCTG GCAGAGACCG AGCCAGAAAAG GCACTTGGGG 300
 TCTTATCTGT TGGACTCTGA AAACACTTCA GCGCCCTTC CAAGGCTTCC CCAAACCCCT 360
 AAGCAGCCGC AGAAGCGCTC CCGAGCTGCC TTCTCCCACA CTCAGGTGAT CGAGTTGGAG 420
 AGGAAGTTCA GCCATCAGAA GTACCTGTCG GCCCTGAAC GGGCCACCT GGCCAAGAAC 480
 CTCAAGCTCA CGGAGACCCA AGTGAAGATA TGGTTCCAGA ACAGACGCTA TAAGACTAAG 540
 CGAAAGCAGC TCTCCTCGGA GCTGGGAGAC TTGGAGAAGC ACTCCTCTTT GCCGGCCCTG 600
 AAAGAGGAGG CCTTCTCCCG GGCCTCCCTG GTCTCCGTGT ATAACAGCTA TCCTTACTAC 660
 CCATACCTGT ACTGCGTGGG CAGCTGGAGC CCAGCTTTTG GGTA 705

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Arg	Val	Pro	Glu	Pro	Arg	Pro	Gly	Glu	Ala	Lys	Ala	Glu	Gly	1	5	10	15
Ala	Ala	Pro	Pro	Thr	Pro	Ser	Lys	Pro	Leu	Thr	Ser	Phe	Leu	Ile	Gln	20	25	30	
Asp	Ile	Leu	Arg	Asp	Gly	Ala	Gln	Arg	Gln	Gly	Gly	Arg	Thr	Ser	Ser	35	40	45	
Gln	Arg	Gln	Arg	Asp	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Gly	50	55	60	
Gly	Arg	Ser	Arg	Ala	Gly	Ala	Gln	Asn	Asp	Gln	Leu	Ser	Thr	Gly	Pro	65	70	75	80
Arg	Ala	Ala	Pro	Glu	Glu	Ala	Glu	Thr	Leu	Ala	Glu	Thr	Glu	Pro	Glu	85	90	95	
Arg	His	Leu	Gly	Ser	Tyr	Leu	Leu	Asp	Ser	Glu	Asn	Thr	Ser	Gly	Ala	100	105	110	
Leu	Pro	Arg	Leu	Pro	Gln	Thr	Pro	Lys	Gln	Pro	Gln	Lys	Arg	Ser	Arg	115	120	125	
Ala	Ala	Phe	Ser	His	Thr	Gln	Val	Ile	Glu	Leu	Glu	Arg	Lys	Phe	Ser	130	135	140	

His	Gln	Lys	Tyr	Leu	Ser	Ala	Pro	Glu	Arg	Ala	His	Leu	Ala	Lys	Asn
145					150					155					160
Leu	Lys	Leu	Thr	Glu	Thr	Gln	Val	Lys	Ile	Trp	Phe	Gln	Asn	Arg	Arg
				165					170					175	
Tyr	Lys	Thr	Lys	Arg	Lys	Gln	Leu	Ser	Ser	Glu	Leu	Gly	Asp	Leu	Glu
			180					185					190		
Lys	His	Ser	Ser	Leu	Pro	Ala	Leu	Lys	Glu	Glu	Ala	Phe	Ser	Arg	Ala
		195					200					205			
Ser	Leu	Val	Ser	Val	Tyr	Asn	Ser	Tyr	Pro	Tyr	Tyr	Pro	Tyr	Leu	Tyr
	210					215					220				
Cys	Val	Gly	Ser	Trp	Ser	Pro	Ala	Phe	Gly						
225					230										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCTCAGGG TTCCGAGACC GCGGCCCGGG GAGGCGAAAG CGGAGGGGGC CGCGCCGCCG	60
ACCCCGTCCA AGCCGCTCAC GTCCTTCCTC ATCCAGGACA TCCTGCGGGA CGGCGCGCAG	120
CGGCAAGGCG GCCGCACGAG CAGCCAGAGA CAGTGCAGCC CGGAGCCGGA GCCAGAGCCA	180
GAGCCAGAGG GAGGACGCAG CCGCGCCGGG GCGCAGAACG ACCAGCTGAG CACCGGGCCC	240
CGCGCCGCGC CGGAGGAGGC CGAGACGCTG GCAGAGACCG AGCCAGAAAG GCACTTGGGG	300
TCTTATCTGT TGGACTCTGA AAACACTTCA GCGGCCCTTC CAAGGCTTCC CCAAACCCCT	360
AAGCAGCCGC AGAAGCGCTC CCGAGCTGCC TTCTCCCACA CTCAGGTGAT CGAGTTGGAG	420
AGGAAGTTCA GCCATCAGAA GTACCTGTCG GCCCCTGAAC GGGCCACCT GGCCAAGAAC	480
CTCAAGCTCA CGGAGACCCA AGTGAAGATA TGGTTCCAGA ACAGACGCTA TAAGACTAAG	540
CGAAAGCAGC TCTCCTCGGA GCTGGGAGAC TTGGAGAAGC ACTCCTCTTT GCCGGCCCTG	600
AAAGAGGAGG CCTTCTCCCG GGCCTCCCTG GTCTCCGTGT ATAACAGCTA TCCTTACTAC	660
CCATACCTGT ACTGCGTGGG CAGCTGGAGC CCAGCTTTTG GGTAAG	705

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Arg	Val	Pro	Glu	Pro	Arg	Pro	Gly	Glu	Ala	Lys	Ala	Glu	Gly	
1				5					10					15		
Ala	Ala	Pro	Pro	Thr	Pro	Ser	Lys	Pro	Leu	Thr	Ser	Phe	Leu	Ile	Gln	
			20					25					30			
Asp	Ile	Leu	Arg	Asp	Gly	Ala	Gln	Arg	Gln	Gly	Gly	Arg	Thr	Ser	Ser	
		35					40					45				
Gln	Arg	Gln	Cys	Asp	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Gly	
	50					55				60						
Gly	Arg	Ser	Arg	Ala	Gly	Ala	Gln	Asn	Asp	Gln	Leu	Ser	Thr	Gly	Pro	
65					70					75					80	
Arg	Ala	Ala	Pro	Glu	Glu	Ala	Glu	Thr	Leu	Ala	Glu	Thr	Glu	Pro	Glu	
				85					90					95		
Arg	His	Leu	Gly	Ser	Tyr	Leu	Leu	Asp	Ser	Glu	Asn	Thr	Ser	Gly	Ala	
			100					105					110			
Leu	Pro	Arg	Leu	Pro	Gln	Thr	Pro	Lys	Gln	Pro	Gln	Lys	Arg	Ser	Arg	
		115					120					125				
Ala	Ala	Phe	Ser	His	Thr	Gln	Val	Ile	Glu	Leu	Glu	Arg	Lys	Phe	Ser	
		130				135						140				
His	Gln	Lys	Tyr	Leu	Ser	Ala	Pro	Glu	Arg	Ala	His	Leu	Ala	Lys	Asn	
145					150				155						160	
Leu	Lys	Leu	Thr	Glu	Thr	Gln	Val	Lys	Ile	Trp	Phe	Gln	Asn	Arg	Arg	
				165					170					175		
Tyr	Lys	Thr	Lys	Arg	Lys	Gln	Leu	Ser	Ser	Glu	Leu	Gly	Asp	Leu	Glu	
			180					185					190			
Lys	His	Ser	Ser	Leu	Pro	Ala	Leu	Lys	Glu	Glu	Ala	Phe	Ser	Arg	Ala	
		195					200					205				
Ser	Leu	Val	Ser	Val	Tyr	Asn	Ser	Tyr	Pro	Tyr	Tyr	Pro	Tyr	Leu	Tyr	
		210				215					220					
Cys	Val	Gly	Ser	Trp	Ser	Pro	Ala	Phe	Gly							
225					230											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Lys Arg Ser Arg Ala Ala Phe Ser His Ala Gln Val Phe Glu Leu
1 5 10 15
Glu Arg Arg Phe Ala Gln Gln Arg Tyr Leu Ser Gly Pro Glu Arg Ser
20 25 30
Glu Met Ala Lys Ser Leu Arg Leu Thr Glu Thr Gln Val Lys Ile Trp
35 40 45
Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
50 55 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Lys Arg Lys Arg Arg Val Leu Phe Thr Lys Ala Gln Thr Tyr Glu
1 5 10 15
Leu Glu Arg Arg Phe Arg Gln Gln Arg Tyr Leu Ser Ala Pro Glu Arg
20 25 30
Glu His Leu Ala Ser Leu Ile Arg Leu Thr Pro Thr Gln Val Lys Ile
35 40 45
Trp Phe Gln Asn His Arg Tyr Lys Thr Lys Arg Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Arg Lys Pro Arg Val Leu Phe Ser Gln Ala Gln Val Leu Glu Leu
1 5 10 15
Glu Cys Arg Phe Arg Leu Lys Lys Tyr Leu Thr Gly Ala Glu Arg Glu

20 25 30
 Ile Ile Ala Gln Lys Leu Asn Leu Ser Ala Thr Gln Val Lys Ile Trp
 35 40 45

Phe Gln Asn Arg Arg Tyr Lys Ser Lys Arg Gly Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTAACCCT CACTAAAGGG AACAAAAGCT GGAGCTCCAC CGCGGTGGCG GCCGCGTAAT	60
ACGACTCACT ATAGGGCGAA GAATTCGGAT CTATCAATCT GCATCCTTGT TTCAGAACCA	120
TTTGATGTAA GTTTCATAAA TCTTGTGCCT TTGCTCCTAC TTACTTCAGT GTTTATTTCC	180
TAAAAATATT CTCTTGACAC CTGACAGTAC AATGTGCAAT TTCAGTAAAT TTAACATTAA	240
TTCAATACTT CCATCATCGA CCTGACACTG AGACTCATGC CTGTAGTCCT GGCACCTTGA	300
GAGGCCAAGG CAGGAGGATC ACTTGAATCC AGGAAATCGA GGCTGCAGTG AGTTATGATG	360
GCATCACTGC ACTCCAGCCT GGGCGGCAGA GGGAGACCCT GTCCGTAAAA AACAGAAGAG	420
AAAAGACAAG GAAAGAAAAT ACTTCCATCA TCTCTGTTCC ACTTTCGTCT GTTGTACCGG	480
TACCGTCCAG TCCAGTCACA GTACCGGTTG GACCAATCTG GCTAACCCAT TGTTTAGCCA	540
ATGGGTTACA TGTTAACAGT TGGAATCTG CAAAAGAGT ATGCTGATGT TCTTTTGAAC	600
TACTTTTTTA AATGCAGTTT TTGCATTTGT CCCTGGCCTA AAACGCCTTC CATCCGTCTG	660
GAAACTTTTC AAAAGGATGG TATGTCATGT GTCTGGGGAG GAAGGAAAGT TAACAGGTTA	720
TTGCGGATAA AGGAACCACC AAAGAAAACC ACTTCTGCAA CGGGAAAAGG CTTTGGCAAA	780
GGTGTTTTTC TTCTTTCAGC CTGGGGTCTG GCTGCACCTA CTTGTCATGC CTCTTTGAGG	840
TCGTAGATAT TGCAGATCTG AGTTTGCACC ATCTCTCCCA GAGAGAGAGA GCACCCAGAA	900
CTCTCACGGT ACCGCGCGGC TGCAGTGAAT GCGTGCTCAT CCCCTGTAAT TGGCTCTGAC	960
GGTCCTGAAG AGCTAACTGG ACTGTTTGTG TTGATCGTCC CATCCCCAGG AGCTTCTCTC	1020
TGCTGCGGGT GGGTTGGGGC AGAGGAGCCC CGCTTTGGGG TGCCTCCTG GCCTGGGAAA	1080
ACGGCTCAGG GCGGAGGGAG GAGAGCTGGA GAAGGAGAGG AAATTGGGGA AGGAGAGGGA	1140

ATTGGGGAAG GAGAGGGAAC TGGGGAAGGA ATCCCCTAGG GAGGAGCGGA GCGGGGCAGT	1200
GCTCAGGGCT CGCAGATCGG CGGGGTCACC TGGGGCTCAG GGCGGCCAAT CCGCGGCGCG	1260
GCCCGTCCCG CGGCCAATGG GAGGGCGGCG CGGCCCGCTC CCCTGGGCTA TAAGCGAGCC	1320
GGGAGGCGGA AAGTGAAAGC GGTGCGGGCC GGGCGGGTGC ATTCAGGCCA AGGCGGGGCC	1380
GCCGGGATGC TCAGGGTTCC GGAGCCGCGG CCCGGGGAGG CGAAAGCGGA GGGGGCCGCG	1440
CCGCCGACCC CGTCCAAGCC GCTCACGTCC TTCCTCATCC AGGACATCCT GCGGGACGGC	1500
GCGCAGCGGC AAGGCGGCCG CACGAGCAGC CAGAGACAGC GCGACCCGGA GCCGGAGCCA	1560
GAGCCAGAGC CAGAGGGAGG ACGCAGCCGC GCCGGGGCGC AGAACGACCA GCTGAGCACC	1620
GGGCCCCGCG CCGCGCCGGA GGAGGCCGAG ACGCTGGCAG AGACCGAGCC AGGTAAGCGG	1680
CGAGGCCGGG GAAGGGGGGC AGCCCAAGGC GGACCCCAG AGCTCGGGGT GCAGGGACGC	1740
GGGGCTCCGC GGCACAGGC AGAGGGACCT TCCCGCCTCC GCAGCCACGC GCGCGCCCCC	1800
GGAATGAACC CTGAGCCCCA GCGTCAGGGC GGCGCAGGAT TCTGACACCG CAGGATTCGC	1860
CCGGTTCCGT GCCTTCCGTT CCCTGGGGCT CAGAAGCCGG CGCGACTGCA GCGCCACCGC	1920
CTTCCACCGT CCCAGGAGCG GATCCCGCCC CGCGCCACCC GCGATCGGCG CCAGCCCCCC	1980
GGTAGTTATG AGAANTAATA ATAATTATT AACAGTGACA AAGCAGGGGT TGACCAGCAA	2040
AGCCTCCGTG TGCTTCCCAA TCCCGTGGGC AGTAAAGCGG TATATTCGGG GTTCCCTCCG	2100
GTGTCCAGGA GAGAGAGTCC ACTTATTTTC TTTCTGTCA CTTCTGATGA GGCGACCGAA	2160
CGCCTCGTTT AGCGAAGAGG GAATTAAAGC CCAGAATGAG CCTGCCTCTG CGTCTCCAGT	2220
GGCACAAGCC CTCTCTTGCC CACCTGGATC CTAACACCGG ATGTCTTTTG GTCTGGCCTT	2280
CCCGGGTATC TTGTTCCACG GCATTTTCCC TGCTCCCTC TCCCGCCTCT CCTCAGCACA	2340
CAGATCCAGA ATCCCCATAT AATTCTACTA GACAGTAGGG AGAAAGTTCA ACCACGAAAC	2400
GTCTCTAACT TTGGGTCTT GATGATTCTT AGCAAATGAA TGCGTAATAA ACATATTTAC	2460
TCACTCTTCA CTCCGGAGAG CTCCTTAGTC ATGTGAAAAA AGTGAAATGT ATCCACGATG	2520
ACAGTGGGCT GTTTGTTTAC TACTAAAGA GATAAGGGTG GATTGAATTC TCTTCTCTTC	2580
CCTGCTAACA TGTAACTTTT GTCTTCCCAT CCCTCCTTCC CCACTCTCCT TTCCAGAAAG	2640
GCACTTGGGG TCTTATCTGT TGGACTCTGA AAACACTTCA GGCGCCCTTC CAAGGCTTCC	2700
CCAAACCCCT AAGCAGCCGC AGAAGCGCTC CCGAGCTGCC TTCTCCACA CTCAGGTGAT	2760
CGAGTTGGAG AGGAAGTTCA GCCATCAGAA GTACCTGTCTG GCCCCTGAAC GGGCCCACCT	2820
GGCCAAGAAC CTCAAGCTCA CGGAGACCCA AGTGAAGATA TG GTTCCAGA ACAGACGCTA	2880
TAAGACTAAG CGAAAGCAGC TCTCCTCGGA GCTGGGAGAC TTGGAGAAGC ACTCCTCTTT	2940
GCCGGCCCTG AAAGAGGAGG CCTTCTCCCG GGCCTCCCTG GTCTCCGTGT ATAACAGCTA	3000

TCCTTACTAC CCATACCTGT ACTGCGTGGG CAGCTGGAGC CCAGCTTTTG GGTAATGCCA 3060
GCTCAGGTGA CAACCATTAT GATCAAAAAC TGCCTTCCCC AGGGTGTCTC TATGAAAAGC 3120
ACAAGGGGCC AAGGTCAGGG AGCAAGAGGT GTGCACACCA AAGCTATTGG AGATTGCGT 3180
GGAAATCTCA GATTCTTCAC TGGTGAGACA ATGAAACAAC AGAGACAGTG AAAGTTTTAA 3240
TACCTAAGTC ATTCCTCCAG TGCATACTGT AGGTCATTTT TTTTGGTTCT GGCTACCTGT 3300
TTGAAGGGGA GAGAGGGAAA ATCAAGTGGT ATTTTCCAGC ACTTTGTATG ATTTTGGATG 3360
AGTTGTACAC CCAAGGATTC TGTTATGCAA CTCCATCCTC CTGTGTCAC GAATATCAAC 3420
TCTGAAAGAG CAAACCTAAC AGGAGAAAGG ACAACCAGGA TGAGGATGTC ACCAACTGAA 3480
TTAAACTC 3488

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu Arg Val Ala Glu Pro Arg Glu Pro Arg Val Glu Ala Gly Gly
1 5 10 15
Arg Ser Pro Trp Ala Ala Pro Pro Thr Gln Ser Lys Arg Leu Thr Ser
20 25 30
Phe Leu Ile Gln Asp Ile Leu Arg Asp Arg Ala Glu Arg His Gly Gly
35 40 45
His Ser Gly Asn Pro Gln His Ser Pro Asp Pro Arg Arg Asp Ser Ala
50 55 60
Pro Glu Pro Asp Lys Ala Gly Gly Arg Gly Val Ala Pro Glu Asp Pro
65 70 75 80
Pro Ser Ile Arg His Ser Pro Ala Glu Thr Pro Thr Glu Pro Glu Ser
85 90 95
Asp Ala His Phe Glu Thr Tyr Leu Leu Asp Cys Glu His Asn Pro Gly
100 105 110
Asp Leu Ala Ser Ala Pro Gln Val Thr Lys Gln Pro
115 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Leu Arg Val Pro Glu Pro Arg Pro Gly Glu Ala Lys Ala Glu Gly
1      5      10      15
Ala Ala Pro Pro Thr Pro Ser Lys Pro Leu Thr Ser Phe Leu Ile Asp
20      25      30
Ile Leu Arg Asp Gly Ala Gln Arg Gln Gly Gly Arg Thr Ser Ser Gln
35      40      45
Arg Gln Cys Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gly Gly
50      55      60
Arg Ser Arg Ala Gly Ala Gln Asn Asp Gln Leu Ser Thr Gly Pro Arg
65      70      75      80
Ala Ala Pro Glu Glu Ala Glu Thr Leu Ala Glu Thr Glu Pro Glu Arg
85      90      95
His Leu Gly Ser Tyr Leu Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu
100     105     110
Pro Arg Leu Pro Gln Thr Pro Lys Gln Pro
115     120
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile Glu Leu
1      5      10      15
Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu Arg Ala
20      25      30
His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys Ile Trp
35      40      45
Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
50      55      60
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile Glu Leu
1          5          10          15
Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu Arg Ala
20          25          30
His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys Ile Trp
35          40          45
Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Leu Ser Glu Asp Leu Gly Val Leu Glu Lys Asn Ser Pro Leu Ser Leu
1          5          10          15
Pro Ala Leu Lys Asp Asp Ser Leu Pro Ser Thr Ser Leu Val Ser Val
20          25          30
Tyr Thr Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Leu Gly Ser Trp
35          40          45
His Pro Ser Phe Trp
50

```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
 1 5 10 15
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
 20 25 30
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
 35 40 45
 Ala Phe Gly
 50

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGGATCCA TGCTCAGGGT TCCGGAG

27

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGAGCTTTT ACCCAAAGC TGGGCT

26

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGGATCCC ATGCTCAGGG TTCCGGAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGGATCCTT ACCCAAAAGC TGGGCT

26

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGGATCCTT ACCCAAAAGC TGGGCT

26

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CACTGCCCAG TCAAGTGTTT TTGA

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACTGCCCAG TCACGTGTTT GTGA

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(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACACTAATTG GAGGC

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(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACACTACTTG GAGGC

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTAATGGC TTTTCTC

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCCTG TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC	420
AGCAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCAGAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCT CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGTTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTCGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTG ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTTGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG	1860

CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCGTC	2220
TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCGCGGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTT	2700
GAACCCAGAG GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTC GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTGC	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720

CTCTTTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTACAC ATTAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTACACAT TAAAGAGGAG AAATTACATA TG	112

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCTCGAGCTT TCCACGCAAA TCTCCAATAG CGTTGGTGTG CACACTCTTG CTCCCTGACC	60
TTGGCCCCTT GTGCTTTTCA TAGAGACACC CTGGGGAAGG CAGTTTTTGA TCATAATGGT	120
TGTCACCTGA GCTGGCATT CAAAAAGCT GGGCTCCACT GCCCAGCAG TACAGGTATG	180
GGTAGTAAGG ATAGCTGTTA TACACGGAGA CCAGGGAGGC CCGGGAGAAG GCCTCTCTTT	240
CAGGGCCGGC AAAGAGGAGT GCTTCTCCAA GTCTCCCAGC TCCGAGGAGA GTGCTTTTCG	300
CTTAGTCTTA TAGCGTCTGT TCTGGAACCA TATCTTCACT TGGGTCTCCG TGAGCTTGAG	360
GTTCTTGCC AGGTGGGCGG TTCAGGGCGA TCAGGTACTT CTGATGGCTG AACTT	415

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTTTTTTCCC GTCCGACCCT CCGGAGTTTA TCACTTCCA GCGGTACTGG GCTGGACCGA	60
GCCTTGGTGG CATCCGATTC AGCTCCAGCA GCATCCCAGG TCCTATCCAG CATGGGCGGG	120
GCACCGCTGG TCAGAGCTCT GGCCTTCAGG AATCTTCGGA CTCGTCCCTT TCCTCGAAGT	180
CGGGCTCGGG CTCTGGGTCC GGTCTGGCT CCAGTTCGG CTCTGGTTCT GCTTCAGCCT	240
CGGGTTCCAG CTCTGGCTCT GGCTCCGGCT CCGGTTCAGC CTCTTTAGAG GCCTCAGCTT	300
CCAGCTCTGG CTCTGGCTCC TCCGGGGTCC CGGATTGCAC CGCTCGGAG CGCTCAGGCC	360
CTCCGGCTAC GTCAGGGTCT GAAGCTCTGG GCAACCCGGG GCATGTGGTC ACCGAGCCGG	420
GTGCCTCCGG GTCCAGTGGC CTGGGCATGG AGGGTCATAG CTGCGGTCGC GGTAGCCCGG	480
ACCCACGTAC TGCGAGTCGA AAGCGGG	507

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

NGCACAGCAG NNAGGCACTT GGAGGTCTTA TCTGTTNGAC TTGNTNAACA CTCAGGCGC	60
CCTTCCAAGG CTTCCCCAAA CCCCTAAGCA GCCGCANAAG CGTCCCGAG CTGCCTTCTC	120
CCACACTCAG GTGATCGAGT TGGAGAGGAA GTTCAGCCAT CAGAAGTACC TGTCGGCCCC	180
TGGAACGGGC CCACCTGGCC AAGAACCTCA AGCTCACGGA GACCCAAGTG AAGATATGGT	240
TCCAGAACAG ACGCTATAAG ACTAAGCGAA ACAGCTCTCC TCGGANCTGG GGAGACTTGG	300
AGAAGCACTC CTCTTTGNCC GGCCCTGAAN GAGGAGGCCN TCNCCCGGGC CNNCCTGGTC	360
NCCGTGTAAT AACAGCGANC CTTNANTACC CATACTGTG ANGNTGGGG CANNGGGAAG	420
CCCAGTTTNT TGGTAAANGG CCAGCTCCAG GTGAACAACC ATTAAGGATC AAAANGGCCT	480
TNCCCCAGGG TGTTNCATGG AAAAGCACAA GGGGCAAGGT CAGGAGCAAA AGN	533

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGAGCTGGA GCCAGAGCCA GAGCCAGATC TCAGGAAACT GGGGTCATTG CATAGAGGCT	60
GCCAGACAGT CTGCAGAGCT CAGCGGCCTG GGTTCAAACC TTCTCGCACA CTGCCACTGT	120
CGGTTACTTT GGCTTTCTAG AGCCAGATTC CTTGGCCATG AAATGGGTAC TGCTTACTTC	180
CCAGGTTATT TTGAGAATGA AGTGAGATGA AGTCAACAGT AGATGTATCT GTCCGTTGTC	240
CCTGCCCTGC TGTGGGGATG ACAGAGTGAT TTTGGACAAG ACCCAAGGNC TCGCTGGGCA	300
TCACTGGTCT TTCTTCAG	318